



SEQUENCE LISTING

(1) GENERAL INFORMATION:

B1

(i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 56

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: David A. Jackson, Esq.
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(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

Reb C3
(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/586,594
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-162

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGTTCT CCAGGTTCCA GGCCTCTCG 60
CCATGCCGGA TCAGCACCAAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG TTGCTTGAG 120
AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAAACA CTGAAGGGAA GACACTGGCT 180
TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT AGAGTGCTGG 240
ATGAAAGGGG ACTTGACATT ATTCACTCTGT CATATGGAGC CATTACCTAA GAACCCCTTC 300
AAGAATTATG ACTCTAAGGT CCATCTTTA TATGATCTGC CTGAAGTCAT AGATGATTG 360
CCTCTGCCCG CACTGAAAGA CAGCTTCAG ACTGTCCAAT GCAACTGCAG TCTTCGGGAA 420
TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTTCT GATGTATTTG 480
GAAATCACAT CTGCCGGTGT GAGTTTCAG TCACCTCTGA TGTCACTGCA GCCCATGCTT 540
GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA TGGTAATTAA 600
AAGATTCTT GGGACAGCCA AACAAATGGCA CCATTCCGC TTCAATATCA GGTGAAATAT 660
TTAGAGAATT CTACAATTGT AAGAGAGGCT CCTGAAATTG TCTCAGCTAC ATCTCTGCTG 720
GTAGACAGTG TGCTTCCTGG ATCTTCATAT GAGGTCCAGG TGAGGAGCAA GAGACTGGAT 780
GGTCAGGAG TCTGGAGTGA CTGGAGTTCA CCTCAAGTCT TTACCACACA AGATGTTGTG 840
TATTTCCAC CCAAAATTCT GACTAGTGT GGATCGAATG CTTCTTTCA TTGCATCTAC 900
AAAAACGAAA ACCAGATTAT CTCCTAAAAA CAGATAGTTT GGTGGAGGAA TCTAGCTGAG 960
AAAATCCCTG AGATACAGTA CAGCATTGTG AGTGACCGAG TTAGCAAAGT TACCTCTCC 1020
AACCTGAAAG CCACCAGACC TCGAGGGAAG TTTACCTATG ACGCAGTGTAA CTGCTGCAAT 1080
GAGCAGGCGT GCCATCACCG CTATGCTGAA TTATACGTGA TCGATGTCAA TATCAATATA 1140
TCATGTGAAA CTGACGGGTA CTTAACTAAA ATGACTTGCA GATGGTCACC CAGCACAATC 1200
CAATCACTAG TGGGAAGCAC TGTGCAGCTG AGGTATCACA GGCGCAGCCT GTATTGTCCT 1260
GATAGTCCAT CTATTCATCC TACGTCTGAG CCCAAAAACT GCGTCTTACA GAGAGACGGC 1320
TTTTATGAAT GTGTTTCCA GCCAATCTT CTATTATCTG GCTATACAAT GTGGATCAGG 1380
ATCAAACCATT CTTTAGGTTC ACTTGACTCG CCACCAACGT GTGCTCTTCC TGACTCCGTA 1440
GTAAAACCAC TACCTCCATC TAACGTAAAAA GCAGAGATTA CTGTAAACAC TGGATTATTG 1500
AAAGTATCTT GGGAAAAGCC AGTCTTCCG GAGAATAACC TTCAATTCCA GATTGATAT 1560
GGCTTAAGTG GAAAAGAAAT ACAATGGAAG ACACATGAGG TATTCGATGC AAAGTCAAAG 1620
TCTGCCAGCC TGCTGGTGT AGACCTCTGT GCAGTCTATG TGGTCCAGGT TCGCTGCCGG 1680
CGGTTGGATG GACTAGGATA TTGGAGTAAT TGGAGCAGTC CAGCCTATAC GCTTGTCTG 1740
GATGTAAAAG TTCCTATGAG AGGGCCTGAA TTTTGGAGAA AAATGGATGG GGACGTTACT 1800
AAAAAGGAGA GAAATGTCAC CTTGCTTTGG AAGCCCTGA CGAAAATGA CTCACTGTGT 1860
AGTGTGAGGA GGTACGTGGT GAAGCATCGT ACTGCCACCA ATGGGACGTG GTCAGAAGAT 1920

GTGGGAAATC GGACCAATCT CACTTCCCTG TGGACAGAAC CAGGCCACAC TGTACAGTT	1980
CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTAA ACCTTACCTT CTCATGGCCC	2040
ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC	2100
ATCCTTCCT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG	2160
AAGATCCTTA ATGAAGATGA TGGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTAAAAAAG	2220
TTTTATATCC ACGATAATTT TATTCCCATC GAGAAATATC AGTTTAGTCT TTACCCAGTA	2280
TTTATGGAAG GAGTTGGAAA ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC	2340
AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTC CTCTTGTGTC	2400
CTACTGCTCG GAACACTGTT AATTCACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT	2460
GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC	2520
ACTCTTTGA	2529

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly	Leu	Arg	Ser	Ala	Ser	Tyr	Gln	Pro	Leu	Lys	Arg	Phe	Ser	Arg	Phe
1				5				10						15	

Gln	Ala	Leu	Ser	Pro	Cys	Arg	Ile	Ser	Thr	Ser	Leu	Xaa	Leu	Val	Pro
				20				25					30		

Asn	Ser	Ala	Arg	Gly	Cys	Phe	Gly	Asn	Glu	Gln	Gly	Gln	Asn	Cys	Ser
					35		40					45			

Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	Ser	Val	Val	Lys
	50				55				60						

Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	Ile	Glu	Cys	Trp
	65			70					75				80		

Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	Glu	Pro	Leu	Pro
	85							90					95		

Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	Leu	Leu	Tyr	Asp
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100 105 110

Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser
115 120 125

Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
130 135 140

Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu
145 150 155 160

Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu
165 170 175

Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
180 185 190

Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
195 200 205

Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
210 215 220

Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
225 230 235 240

Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
245 250 255

Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
260 265 270

Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
275 280 285

labeled C37

Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
290 295 300

Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
305 310 315 320

Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
325 330 335

Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
340 345 350

Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
355 360 365

Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
370 375 380

Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
385 390 395 400

Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
405 410 415

Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
420 425 430

Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
435 440 445

Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
450 455 460

Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val
465 470 475 480

Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn
485 490 495

Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn
500 505 510

Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln
515 520 525

Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu
530 535 540

Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg
545 550 555 560

Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr
565 570 575

Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp
580 585 590

Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu
595 600 605

Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
610 615 620

Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp
625 630 635 640

Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His
645 650 655

Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn
660 665 670

Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu
675 680 685

Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp
690 695 700

Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp
705 710 715 720

Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser
725 730 735

Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys
740 745 750

Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro
755 760 765

Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn
770 775 780

Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ser	Ser	Cys	Val	
785					790				795					800	
Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu
				805				810					815		
Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly
				820			825					830			
Leu	Asn	Phe	Gln	Lys	Arg	Thr	Asp	Thr	Leu						
				835			840								

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA	GTGCCAACCGG	GAAGGCTTAA	TTAACCTTTG	GAANTGAGTC	CGAAGAGTCT	60
GGAAGTNTGT	AAGATGGAAG	ATACTATACA	AGATACTTCA	GAGCTGTACA	TTCTTCCAGG	120
GATGTAGGCT	AGCAGTTATT	TCATTAGTAT	ATGTCTATT	TAGAATGGGA	AGAATTAGGA	180
AGATGAATGG	AGCCTGTGTC	TTTCACTACT	CTCCCAGGAG	GTTCCAGAAT	AGCNAAAGTG	240
TCAGCCAGAA	TTCTTGAAGT	CATAGACTGG	AGTTAGAGAT	GAACATAAGC	TCATGTTAAG	300
CCTGGGTTAC	TTCTTATCAT	CCTTAATT	GAAAGCTAAG	AGGGCCTAAC	CATCAAGAAC	360
GTCCTGGAGG	AAAGAATGTT	TTAACGCCA	TTATTCAGTC	AAAGAAATT	AGACTTGAGA	420
GAAATGCTCA	TTTCTTCTCT	CATGATGGCT	CCTTACACCT	TACTTCTACC	GTACGATCCA	480
TGNGGCCCTA	CCCACGCAGG	ATACATGCAT	CTATATGAGA	GTGTCTNCC	CTTCTAACTC	540
AGAGACTCTT	GTTCTAGTCT	GTGNTATAAA	ATTCAGCTTG	TGGAAGCTTT	CTGAGGGGTT	600
GGCAGCATT	AATTTACCT	GCAATAGGTA	AAGGTAATCT	TTTGGGAAGT	GAAGAGTGT	660
ATTAGACATT	TCAGAAAGAA	CAAACAGGAT	TGGGGCTGCT	ATGTGTTCTA	CACAGGAATC	720
TTCCATAACA	CAGAATAATT	TATGTAGATA	GAGACAAGAT	GGAAATGCC	AGGGCCCCAA	780
AATAGCCGCT	GTTATTGTT	AACCTTCAAG	GTGTTCTGTT	TGTTTATCTG	TTTCTTGC	840
AGGATCATCT	TCCAAGCACA	TCCTGGGGGA	ACAGTGGCAG	AGTCACTCGA	GTTCATGAAA	900

CTATGGTGAC	ATCTGAGCTT	CCTTGGTTCT	TCACAGAAC	TAAGCAGTTC	CTTGCTTGC	960
TTGTTAGATG	AGAAAACCTTC	CTTGTCA	TGTCTCTACG	ACTAGAATGG	AAAGCCTTAC	1020
TACTTCCTAT	GTATTCTTAA	TATTTCAAAT	GTCCTAATTA	TGTTTGGCTT	CTCTGTCTTT	1080
AAGGGATTAA	GTCTCTGGAT	TTGAAGAAAT	AAATAAATAA	ATAAAGGAAA	ACTAATTTC	1140
TCGTGCCGGA	TGACTGCTAG	CTGAGCTCAG	GCCTACTGCA	TTCTACATTT	CGACTCTCTC	1200
CCTCTTCCCC	AGTGCTTAG	CACTGGACTG	GGCAGTNCC	GGCCTGGTCT	AACTCCTGTT	1260
TCCTGGTGGG	AATGTATAAT	AAGAACTCCA	TGAGTTCTGG	TATAAACACT	GTGGTCTGTG	1320
TGCTAATTAA	ATCTNGTGT	TCCTACAGCC	CCTGACGAAA	AATGACTCAC	TGTGTAGTGT	1380
GAGGAGGTAC	GTGGTGAAGC	ATCGTACTGC	CCACAATGGG	ACGTGGTCAG	AAGATGTGGG	1440
AAATCGGACC	AATCTCACTT	TCCTGTGGAC	AGAACCA	CACACTGTTA	CAGTCTGGC	1500
TGTCAATTCC	CTCGGCCTT	CCCTTGTGAA	TTTTAACCTT	ACCTTCTCAT	GGCCCATGAG	1560
TAAAGTGAGT	GCTGTGGAGT	CACTCAGTGC	TTATCCCCTG	AGCAGCAGCT	GTGTCATCCT	1620
TTCCCTGGACA	CTGTCACCTG	ATGATTATAG	TCTGTTATAT	CTGGTTATTG	AATGGAAGAT	1680
CCTTAATGAA	GATGATGGAA	TGAAGTGGCT	TAGAATTCCC	TCGAATGTTA	AAAAGTTTA	1740
TATCCACGAT	AATTTTATTC	CCATCGAGAA	ATATCAGTTT	AGTCTTAC	CAGTATTTAT	1800
GGAAGGAGTT	GGAAAACCAA	AGATAATTAA	TGGTTTCACC	AAAGATGCTA	TCGACAAGCA	1860
GCAGAACATGAC	GCAGGGCTGT	ATGTCATTGT	ACCCATAATT	ATTTCCCTCTT	GTGTCCTACT	1920
GCTCGGAACA	CTGTTAATT	CACACCAGAG	AATGAAAAAG	TTGTTTTGGG	ACGATGTTCC	1980
AAACCCCAAG	AATTGTTCC	GGGCACAAGG	ACTGAATTTC	CAAAAGCCTG	AAACATTNGA	2040
GCATCTTTT	ACCAAGCATG	CAGAATCAGT	GATATTGGT	CCTCTTCTTC	TGGAGCCTGA	2100
ACCCATTCA	GAAGAAATCA	GTGTCGATAC	AGCTTGGAAA	AATAAAGATG	AGATGGTCCC	2160
AGCAGCTATG	GTCTCCCTNC	TNNNGGACCAC	ACCAGACCC	GAAAGCAGTT	CTATTGTNT	2220
TAGTGACCAG	TGTAACAGTG	CTAACTTCTC	TGGGTCTCAG	AGCACCCAGG	TAACCTGTGA	2280
GGATGAGTGT	CAGAGACAAC	CCTCAGTTAA	ATATGCAACT	GTGGTCAGCA	ACGATAAAACT	2340
AGTGGAAACT	GATGAAGAGC	AAGGGTTTAT	CCATAGTCCT	GTCAGCAACT	GCATCTCCAG	2400
TAATCATTCC	CCACTGAGGC	AGTCTTCTC	TAGCAGCTCC	TGGGAGACAG	AGGCCAGAC	2460
ATTTTCCCTT	TTATCAGACC	AGCAACCCAC	CATGATTCA	CCACAACTTT	CATTCTCGGG	2520
GTTGGATGAG	CTTTTGGAAC	TGGAGGGAAG	TTTCCTGAA	AAAATCACA	GGGAGNAGTC	2580
TGTCCTGTTAT	CTAGGAGTCA	CCTCCGTCCN	CAGAAGAGAG	AGTGGTGTGC	TTTGACTGG	2640
TGAGGCAGGA	ATCCTGTGCA	CATTCCCAGC	CCAGTGTCTG	TTCAAGTACA	TCAGGATCCT	2700
CCAGGAGAGA	TGCTCACACT	TTGTAGAAA	TAATTGAGT	TTAGGGACCT	CTGGTGAGAA	2760
CTTGGTCCT	AACATGCC	AATTCCAAAC	CTGTTCCACG	CACAGTCACA	AGATAATGGA	2820

GAATAAGATG TGTGACTTAA CTGTGTAA

2848

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 581 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Arg Asp Leu Val Ser Gly Phe Glu Glu Ile Asn Lys Ile Lys Glu
1 5 10 15

Asn Phe Ser Arg Ala Gly Leu Leu Ala Glu Leu Arg Pro Thr Ala Phe
20 25 30

Tyr Ile Ser Thr Leu Ser Leu Phe Pro Ser Ala Leu Ala Leu Asp Trp
35 40 45

Ala Val Pro Gly Leu Val Leu Leu Phe Pro Gly Gly Asn Val Glu Leu
50 55 60

His Glu Phe Trp Tyr Lys His Cys Gly Leu Cys Ala Asn Ile Xaa Cys
65 70 75 80

Phe Leu Gln Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
85 90 95

Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp
100 105 110

Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His
115 120 125

Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn
130 135 140

Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu
145 150 155 160

Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp
165 170 175

Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp
180 185 190

Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser
195 200 205

Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys

210 215 220

Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro
225 230 235 240

Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn
245 250 255

Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val
260 265 270

Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu
275 280 285

Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
290 295 300

Leu Asn Phe Gln Lys Pro Glu Thr Phe Glu Gln Leu Phe Thr Lys His
305 310 315 320

Ala Glu Ser Val Ile Phe Gly Pro Leu Leu Leu Glu Pro Glu Pro Ile
325 330 335

Ser Glu Glu Ile Ser Val Asp Thr Ala Trp Lys Asn Lys Asp Glu Met
340 345 350

Val Pro Ala Ala Met Val Ser Leu Leu Trp Thr Thr Pro Asp Pro Glu
355 360 365

Ser Ser Ser Ile Cys Ile Ser Asp Gln Cys Asn Ser Ala Asn Phe Ser
370 375 380

Gly Ser Gln Ser Thr Gln Val Cys Glu Asp Glu Cys Gln Arg Gln Pro
385 390 395 400

Ser Val Lys Tyr Ala Thr Leu Val Ser Asn Asp Lys Leu Val Glu Thr
405 410 415

Asp Glu Glu Gln Gly Phe Ile His Ser Pro Val Ser Asn Cys Ile Ser
420 425 430

Ser Asn His Ser Pro Leu Arg Gln Ser Phe Ser Ser Ser Trp Glu
435 440 445

Thr Glu Ala Gln Thr Phe Phe Leu Leu Ser Asp Gln Gln Pro Thr Met
450 455 460

Ile Ser Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu
465 470 475 480

Glu Gly Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr
485 490 495

Leu Gly Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr
500 505 510

Gly Glu Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser
515 520 525

Asp Ile Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn
530 535 540

Leu Ser Leu Gly Thr Ser Gly Glu Asn Phe Gly Pro Tyr Met Pro Gln
545 550 555 560

Phe Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met
565 570 575

Cys Asp Phe Thr Val
580

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 961 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT	60
TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTCGACTCT	120
CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT	180
GTTCCTGGT GGGATGTAT AATAAGAACT COATGAGTTC TGGTATAAAC ACTGTGGTCT	240
GTGTGCTAAT TAAATCTNGT GTTCCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG	300
TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCCACAAT GGGACGTGGT CAGAAGATGT	360
GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT	420
GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTAAAC CTTACCTTCT CATGGCCCAT	480
GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTAT	540
CCTTCCTGG ACACGTGTCAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA	600
GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAAATT CCCTCGAATG TTAAAAAGTT	660
TTATATCCAC GATAATTAA TTCCCACATCGA GAAATATCAG TTTAGTCTTT ACCCAAGTATT	720
TATGGAAGGA GTTGGAAAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA	780
GCAGCAGAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTTCT CTTGTGTCT	840
ACTGCTCGGA ACACGTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTT GGGACGATGT	900
TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGAATGAAAT TTCCAAAAGG TCACTGTTA	960
A	961

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Arg Asp Leu Val Ser Gly Phe Glu Glu Ile Asn Lys Xaa Ile Lys
1 5 10 15

Glu Asn Xaa Phe Ser Arg Ala Gly Xaa Leu Leu Ala Glu Leu Arg Pro
20 25 30

Thr Ala Phe Tyr Ile Ser Thr Leu Ser Leu Phe Pro Ser Ala Leu Ala
35 40 45

Leu Asp Trp Ala Val Pro Gly Leu Val Xaa Leu Leu Phe Pro Gly Gly
50 55 60

Asn Val Xaa Xaa Glu Leu His Glu Phe Trp Tyr Lys His Cys Gly Leu
65 70 75 80

Cys Ala Asn Xaa Ile Xaa Cys Phe Leu Gln Pro Leu Thr Lys Asn Asp
85 90 95

Ser Leu Cys Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His
100 105 110

Asn Gly Thr Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe
115 120 125

Leu Trp Thr Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser
130 135 140

Leu Gly Ala Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met
145 150 155 160

Ser Lys Val Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser
165 170 175

Ser Cys Val Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu
180 185 190

Leu Tyr Leu Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met
195 200 205

Lys Trp Leu Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp
210 215 220

Asn Phe Ile Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe

225	230	235	240													
Met	Glu	Gly	Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	
				245				250						255		
Ala	Ile	Ile	Asp	Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro
				260				265						270		
Ile	Ile	Ile	Ser	Ser	Cys	Val		Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser
				275				280						285		
His	Gln	Arg	Met	Lys	Lys	Leu		Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys
				290								300				
Asn	Cys	Ser	Trp	Ala	Gln	Gly		Leu	Asn	Phe	Gln	Lys	Val	Thr	Val	
				305								315				

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 2703 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC	AGAAATTCTA	TGTGGTTTG	TTACACTGGG	AATTTCTTTA	TGTGATAGCT	60
GCACCTAAC	TGGCATATCC	AATCTCTCCC	TGGAAATTAA	AGTTGTTTG	TGGACCACCG	120
AACACAAACG	ATGACTCCTT	TCTCTCACCT	GCTGGAGCCC	CAAACAATGC	CTCGGCTTTG	180
AAGGGGGCTT	CTGAAGCAAT	TGTTGAAGCT	AAATTAAATT	CAAGTGGTAT	CTACGTTCT	240
GAGTTATCCA	AAACAGTCTT	CCACTGTTGC	TTTGGGAATG	AGCAAGGTCA	AAACTGCTCT	300
GCACTCACAG	ACAACACTGA	AGGGAAGACA	CTGGCTTCAG	TAGTGAAGGC	TTCAGTTTT	360
CGCCAGCTAG	GTGTAAACTG	GGACATAGAG	TGCTGCATGA	AAGGGGACTT	GACATTATTC	420
ATCTGTCATA	TGGAGCCATT	ACCTAAGAAC	CCCTTCAAGA	ATTATGACTC	TAAGGTCCAT	480
CTTTTATATG	ATCTGCCTGA	AGTCATAGAT	GATTGCCTC	TGCCCCCACT	GAAAGACAGC	540
TTTCAGACTG	TCCAATGCAA	CTGCAGTCTT	CGGGGATGTG	AATGTCATGT	GCCGGTACCC	600
AGAGCCAAAC	TCAACTACGC	TCTTCTGATG	TATTTGGAAA	TCACATCTGC	CGGTGTGAGT	660
TTTCAGTCAC	CTCTGATGTC	ACTGCAGCCC	ATGCTTGTG	TGAAACCCGA	TCCACCCCTTA	720
GGTTTGCATA	TGGAAGTCAC	AGATGATGGT	AATTTAAAGA	TTTCTTGGGA	CAGCCAAACA	780

ATGGCACCAT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA 840
GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT 900
TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG 960
AGTTCACCTC AAGTCTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT 1020
AGTGTGGAT CGAATGCTTC TTTTCATTGC ATCTACAAAA ACGAAAACCA GATTATCTCC 1080
TCAAAACAGA TAGTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC 1140
ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA 1200
GGGAAGTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCGTGCCA TCACCGCTAT 1260
GCTGAATTAT ACGTGATCGA TGTCAATATC AATATATCAT GTGAAACTGA CGGGTACTTA 1320
ACTAAAATGA CTTGCAGATG GTCACCCAGC ACAATCCAAT CACTAGTGGG AAGCACTGTG 1380
CAGCTGAGGT ATCACAGGCG CAGCCTGTAT TGTCCTGATA GTCCATCTAT TCATCCTACG 1440
TCTGAGGCCA AAAACTGCGT CTTACAGAGA GACGGCTTTT ATGAATGTGT TTTCCAGCCA 1500
ATCTTTCTAT TATCTGGCTA TACAATGTGG ATCAGGATCA ACCATTCTT AGGTTCACTT 1560
GACTCGCCAC CAACGTGTGT CCTTCCTGAC TCCGTAGTAA AACCACTACC TCCATCTAAC 1620
GTAAAAGCAG AGATTACTGT AAACACTGGA TTATTGAAAG TATCTTGGGA AAAGCCAGTC 1680
TTTCCGGAGA ATAACCTTCA ATTCCAGATT CGATATGGCT TAAGTGGAAA AGAAATACAA 1740
TGGAAAGACAC ATGAGGTATT CGATGCAAAG TCAAAGTCTG CCAGCCTGCT GGTGTCAGAC 1800
CTCTGTGCAG TCTATGTGGT CCAGGTTCGC TGCCGGCGGT TGGATGGACT AGGATATTGG 1860
AGTAATTGGA GCAGTCCAGC CTATACGCTT GTCATGGATG TAAAAGTTCC TATGAGAGGG 1920
CCTGAATTTC GGAGAAAAAT GGATGGGGAC GTTACTAAAA AGGAGAGAAA TGTCACCTTG 1980
CTTTGGAAGC CCCTGACGAA AAATGACTCA CTGTGTAGTG TGAGGAGGTA CGTGGTGAAG 2040
CATCGTACTG CCCACAATGG GACGTGGTCA GAAGATGTGG GAAATCGGAC CAATCTCACT 2100
TCCCTGTGGA CAGAACCAAGC GCACACTGTT ACAGTTCTGG CTGTCAATTG CCTCGGCGCT 2160
TCCCTGTGA ATTTAACCT TACCTTCTCA TGGCCCATGA GTAAAGTGTAG TGCTGTGGAG 2220
TCACTCAGTG CTTATCCCCT GAGCAGCAGC TGTGTCAATTG TTTCCCTGGAC ACTGTCACCT 2280
GATGATTATA GTCTGTTATA TCTGGTTATT GAATGGAAGA TCCTTAATGA AGATGATGGA 2340
ATGAAGTGGC TTAGAATTCC CTCGAATGTT AAAAGTTTT ATATCCACGA TAATTTATT 2400
CCCATCGAGA AATATCAGTT TAGTCTTAC CCAGTATTTA TGGAAGGAGT TGGAAAACCA 2460
AAGATAATTAA ATGGTTTCAC CAAAGATGCT ATCGACAAGC AGCAGAAATGA CGCAGGGCTG 2520
TATGTCATTG TACCCATAAT TATTCCTCT TGTGTCAATTG TGCTCGGAAC ACTGTTAATT 2580
TCACACCAGA GAATGAAAAA GTTGTGTTGG GACCGATGTTC CAAACCCAA GAATTGTTCC 2640
TGGGCACAAG GACTGAATTG CCAAAAGGAT ATATCTTAC ATGAAGTTTT TATTTTCAGA 2700

TAG

2703

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu	
1									10						15	
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys	
							20		25					30		
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu	
							35		40					45		
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser	
							50		55					60		
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro	
							65		70					80		
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly	
							85		90					95		
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	
							100		105					110		
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	
							115		120					125		
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	
							130		135					140		
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	
							145		150					155		160
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	
							165		170					175		
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	
							180		185					190		
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	
							195		200					205		

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
210 215 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
225 230 235 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
245 250 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
260 265 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
275 280 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
290 295 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
305 310 315 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
325 330 335

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
355 360 365

Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
370 375 380

Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
385 390 395 400

Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
405 410 415

His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
420 425 430

Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
435 440 445

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
450 455 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
465 470 475 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
485 490 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
500 505 510

Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
515 520 525

Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
530 535 540

Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val

545 550 555 560
Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
565 570 575
Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
580 585 590
Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
595 600 605
Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
610 615 620
Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
625 630 635 640
Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
645 650 655
Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
660 665 670
Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
675 680 685
Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
690 695 700
Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
705 710 715 720
Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
725 730 735
Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
740 745 750
Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
755 760 765
Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
770 775 780
Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
785 790 795 800
Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
805 810 815
Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp
820 825 830
Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile
835 840 845
Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
850 855 860
Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
865 870 875 880
Trp Ala Gln Gly Leu Asn Phe Gln Lys Asp Ile Ser Leu His Glu Val
885 890 895

Phe Ile Phe Arg
900

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: A20 (OB-Re)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGGAATCGT	TCTGCAAATC	CAGGTGTACA	CCTCTGAAGA	AAGATGATGT	GTCAGAAATT	60
CTATGTGGTT	TTGTTACACT	GGGAATTCT	TTATGTGATA	GCTGCACTTA	ACCTGGCATA	120
TCCAATCTCT	CCCTGGAAAT	TTAAGTTGTT	TTGTGGACCA	CCGAACACAA	CCGATGACTC	180
CTTCTCTCA	CCTGCTGGAG	CCCCAAACAA	TGCCTCGGCT	TTGAAGGGGG	CTTCTGAAGC	240
AATTGTTGAA	GCTAAATTTA	ATTCAAGTGG	TATCTACGTT	CCTGAGTTAT	CCAAAACAGT	300
CTTCCACTGT	TGCTTTGGGA	ATGAGCAAGG	TCAAAACTGC	TCTGCACTCA	CAGACAACAC	360
TGAAGGGAAG	ACACTGGCTT	CAGTAGTGAA	GGCTTCAGTT	TTTCGCCAGC	TAGGTGTAAA	420
CTGGGACATA	GAGTGCTGGA	TGAAAGGGGA	CTTGACATTA	TTCATCTGTC	ATATGGAGCC	480
ATTACCTAAG	AACCCCTTCA	AGAATTATGA	CTCTAAGGTC	CATCTTTAT	ATGATCTGCC	540
TGAAGTCATA	GATGATTCGC	CTCTGCCCCC	ACTGAAAGAC	AGCTTTCAGA	CTGTCCAATG	600
CAACTGCAGT	CTTCGGGGAT	GTGAATGTCA	TGTGCCGGTA	CCCAGAGCCA	AACTCAACTA	660
CGCTCTTCTG	ATGTATTTGG	AAATCACATC	TGCCGGTGTG	AGTTTCAGT	CACCTCTGAT	720
GTCACTGCAG	CCCATGCTTG	TTGTGAAACC	CGATCCACCC	TTAGGTTGC	ATATGGAAGT	780
CACAGATGAT	GGTAATTAA	AGATTCTTG	GGACAGCCAA	ACAATGGCAC	CATTCCGCT	840
TCAATATCAG	GTGAAATATT	TAGAGAATTTC	TACAATTGTA	AGAGAGGCTG	CTGAAATTGT	900
CTCAGCTACA	TCTCTGCTGG	TAGACAGTGT	GCTTCCTGGA	TCTTCATATG	AGGTCCAGGT	960
GAGGAGCAAG	AGACTGGATG	GTTCAGGAGT	CTGGAGTGAC	TGGAGTTCAC	CTCAAAGTCTT	1020
TACCAACACAA	GATGTTGTGT	ATTTCCACC	CAAAATTCTG	ACTAGTGTG	GATCGAATGC	1080
TTCTTTTCAT	TGCATCTACA	AAAACGAAAAA	CCAGATTATC	TCCTCAAAAC	AGATAGTTG	1140

GTGGAGGAAT	CTAGCTGAGA	AAATCCCTGA	GATACAGTAC	AGCATTGTGA	GTGACCGAGT	1200
TAGCAAAGTT	ACCTTCTCCA	ACCTGAAAGC	CACCAGACCT	CGAGGGAAAGT	TTACCTATGA	1260
CGCAGTGTAC	TGCTGCAATG	AGCAGGGCTG	CCATCACCGC	TATGCTGAAT	TATACGTGAT	1320
CGATGTCAAT	ATCAATATAT	CATGTGAAAC	TGACGGGTAC	TTAACTAAAA	TGACTTGCAG	1380
ATGGTCACCC	AGCACAAATCC	AATCACTAGT	GGGAAGCACT	GTGCAGCTGA	GGTATCACAG	1440
GCGCAGCCTG	TATTGTCCTG	ATAGTCCATC	TATTCATCCT	ACGTCTGAGC	CCAAAAACTG	1500
CGTCTTACAG	AGAGACGGCT	TTTATGAATG	TGTTTCCAG	CCAATCTTC	TATTATCTGG	1560
CTATACAATG	TGGATCAGGA	TCAACCATTG	TTTAGGTTCA	CTTGACTCGC	CACCAACGTG	1620
TGTCCTTCCT	GAECTCGTAG	TAAAACCCT	ACCTCCATCT	AACGTAAAAG	CAGAGATTAC	1680
TGTAAACACT	GGATTATTGA	AAAGTATCTTG	GGAAAAGCCA	GTCTTCCGG	AGAATAACCT	1740
TCAATTCCAG	ATTGATGATG	GCTTAAGTGG	AAAAGAAATA	CAATGGAAGA	CACATGAGGT	1800
ATTGATGCA	AAGTCAAAGT	CTGCCAGCCT	GCTGGTGTCA	GACCTCTGTG	CAGTCTATGT	1860
GGTCCAGGTT	CGCTGCCGGC	GGTTGGATGG	ACTAGGATAT	TGGAGTAATT	GGAGCAGTCC	1920
AGCCTATACG	CTTGTATGG	ATGTAAAAGT	TCCTATGAGA	GGGCCTGAAT	TTTGGAGAAA	1980
AATGGATGGG	GACGTTACTA	AAAAGGAGAG	AAATGTCACC	TTGCTTGGG	AGCCCCGTGAC	2040
GAAAAATGAC	TCACTGTGTA	GTGTGAGGAG	GTACGTGGTG	AAGCATCGTA	CTGCCACAA	2100
TGGGACGTGG	TCAGAAGATG	TGGGAAATCG	GACCAATCTC	ACTTCCTGT	GGACAGAACCC	2160
AGCGCACACT	GTTACAGTTC	TGGCTGTCAA	TTCCCTCGGC	GCTTCCCTTG	TGAATTTAA	2220
CCTTACCTTC	TCATGGCCCA	TGAGTAAAGT	GAGTGCTGTG	GAGTCACTCA	GTGCTTATCC	2280
CCTGAGCAGC	AGCTGTGTCA	TCCTTCCTG	GACACTGTCA	CCTGATGATT	ATAGTCTGTT	2340
ATATCTGGTT	ATTGAATGGA	AGATCCTAA	TGAAGATGAT	GGAATGAAGT	GGCTTAGAAT	2400
TCCCTCGAAT	GTTAAAAGT	TTTATATCCA	CGGTATGTGT	ACTGTACTTT	TCATGGATTA	2460
G						2461

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 805 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
20 25 30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
35 40 45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
50 55 60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65 70 75 80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
85 90 95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
100 105 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
115 120 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
130 135 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
145 150 155 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
165 170 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
180 185 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
195 200 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
210 215 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
225 230 235 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
245 250 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
260 265 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
275 280 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
290 295 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
305 310 315 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
325 330 335

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
355 360 365

Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
370 375 380

Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
385 390 395 400

Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
405 410 415

His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
420 425 430

Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
435 440 445

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
450 455 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
465 470 475 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
485 490 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
500 505 510

Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
515 520 525

Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
530 535 540

Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
545 550 555 560

Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
565 570 575

Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
580 585 590

Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
595 600 605

Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
610 615 620

Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
625 630 635 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
645 650 655

Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys

660	665	670
Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr		
675	680	685
Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr		
690	695	700
Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala		
705	710	715
Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val		
725	730	735
Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val		
740	745	750
Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu		
755	760	765
Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu		
770	775	780
Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Gly Met Cys Thr		
785	790	795
Val Leu Phe Met Asp		
805		

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Phe Gln Lys Arg Thr Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln	Leu	Phe	Thr	Lys	His	Ala
1				5				10					15		
Glu	Ser	Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile	Ser
			20				25					30			
Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met	Val
	35				40				45						
Pro	Ala	Ala	Met	Val	Ser	Leu	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu	Ser
	50				55				60						
Ser	Ser	Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser	Gly
	65				70				75				80		
Ser	Gln	Ser	Thr	Gln	Val	Cys	Glu	Asp	Glu	Cys	Gln	Arg	Gln	Pro	Ser
			85				90				95				
Val	Lys	Tyr	Ala	Thr	Leu	Val	Ser	Asn	Asp	Lys	Leu	Val	Glu	Thr	Asp
	100					105						110			
Glu	Glu	Gln	Gly	Phe	Ile	His	Ser	Pro	Val	Ser	Asn	Cys	Ile	Ser	Ser
	115					120					125				
Asn	His	Ser	Pro	Leu	Arg	Gln	Ser	Phe	Ser	Ser	Ser	Ser	Trp	Glu	Thr
	130				135					140					
Glu	Ala	Gln	Thr	Phe	Phe	Leu	Leu	Ser	Asp	Gln	Gln	Pro	Thr	Met	Ile
	145				150				155			160			
Ser	Pro	Gln	Leu	Ser	Phe	Ser	Gly	Leu	Asp	Glu	Leu	Leu	Glu	Leu	Glu
			165				170					175			
Gly	Ser	Phe	Pro	Glu	Glu	Asn	His	Arg	Glu	Lys	Ser	Val	Cys	Tyr	Leu
			180				185				190				
Gly	Val	Thr	Ser	Val	Asn	Arg	Arg	Glu	Ser	Gly	Val	Leu	Leu	Thr	Gly
	195				200				205						
Glu	Ala	Gly	Ile	Leu	Cys	Thr	Phe	Pro	Ala	Gln	Cys	Leu	Phe	Ser	Asp
	210				215					220					
Ile	Arg	Ile	Leu	Gln	Glu	Arg	Cys	Ser	His	Phe	Val	Glu	Asn	Asn	Leu
	225				230				235				240		
Ser	Leu	Gly	Thr	Ser	Gly	Glu	Asn	Phe	Gly	Pro	Tyr	Met	Pro	Gln	Phe
			245				250				255				

Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys
260 265 270

Asp Phe Thr Val
275

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Phe Gln Lys Val Thr Val
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Phe Gln Lys Asp Ile Ser His Glu Val Phe Ile Phe Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Tyr Ile His Gly Met Cys Thr Val Leu Phe Met Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

12

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTTA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAAC CTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
1 5 10 15

Ser Glu Pro Lys
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln Arg Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn
1 5 10 15

Cys Ser Trp

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG CCGAGGGAAT TGACAGCCAG AACTGTAACA GTGTGCGCTG GTTCTGTCCA	60
CAGGAAAGTG AGATTGGTCC GATTCCCAC ATCTTCTGAC CACGTCCCAC TGTGGGCAGT	120
ACGATGCTTC ACCACGTACC TCCTCACACT ACACAGTGAG TCATTT	166

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCA ACAATGGGAC GTGGTCAGAA GATGTGGGAA ATCGGACCAA	60
TCTCACTTTC CTGTGGACAG AACCAAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCCT	120
CGGCGCTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC	180
TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT	240
GTCACCTGAT GATTATAGTC TGTTATATCT GGTTATTGAA TGGAAAGATCC TTAATGAAGA	300
TGATGGAATG AAGTGGCTTA	320

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG CTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT	60
CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT	120
CATCCTCACA GGTTACCTGG GTGCTCTGAG ACCCAGAG	158

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAGGCTC TGTGTTCATT TGATGTTCAG	60
AAGTCAGCAA GGTTCTCATA TGTCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG	120
CTAACAAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACACTACTTG GTGTTTTACT	180
TAAAGATACG AG	192

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGACTGACAA GGAAGTTTC TCATCTAACAA AGCAAGCAAA GGAAGTGCCTT ATGTNCTGTG	60
ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT	120
GTTCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGAACAGATA	168

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATTATGA CTCTAAGGTC CATCTTTAT ATGATCTGCC TGAAGTCATA GATGATTCCG	60
CTCTGCCCTT ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTGGGGAT	120
GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTTGG	180
NAATCACATC TGCCGGTGTG AGTTTCAGT CACCTCTGAT GTCACTGCAG CCCATGCTTG	240
TTTGAAACC CGATCCACC	259

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTGGG GCTCCAGCAG	60
GTGAGAGAGAA GGAGTCATCG GTTGTGTTCG GTGGTCCACA AAACAACTTA AATTCCAGG	120
GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAACA	180
AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTCAG	240
AACGATTCCCT	250

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC	18
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(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG	22
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(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

· (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCAAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

· (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

· (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTCTGC CTTCCTTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTCT TGCGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATT CGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCACTG

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 894 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-R

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1 5 10 15

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
20 25 30

Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
35 40 45

Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
50 55 60

Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65 70 75 80

Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
85 90 95

Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
100 105 110

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
115 120 125

Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
130 135 140

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
145 150 155 160

Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
165 170 175

Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
180 185 190

Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
195 200 205

Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
210 215 220

Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
225 230 235 240

Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
245 250 255

Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
260 265 270

Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
275 280 285

Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
290 295 300

Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
305 310 315 320

Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
325 330 335

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
340 345 350

Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
355 360 365

Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
370 375 380

Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
385 390 395 400

Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
405 410 415

His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
420 425 430

Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
435 440 445

Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
450 455 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
465 470 475 480

Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
485 490 495

Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
500 505 510

Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
515 520 525

Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
530 535 540

Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
545 550 555 560

Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
565 570 575

Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
580 585 590

Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
595 600 605

Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
610 615 620

Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
625 630 635 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
645 650 655

Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
660 665 670

Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
675 680 685

Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr

690 695 700
 Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
 705 710 715 720
 Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
 725 730 735
 Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
 740 745 750
 Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
 755 760 765
 Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
 770 775 780
 Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
 785 790 795 800
 Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
 805 810 815
 Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp
 820 825 830
 Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile
 835 840 845
 Ser Ser Cys Val Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
 850 855 860
 Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
 865 870 875 880
 Trp Ala Gln Gly Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
 885 890

"(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1165 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Ile Cys Gln Lys Phe Cys Val Val Leu Leu His Trp Glu Phe Ile
 1 5 10 15
 Tyr Val Ile Thr Ala Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg
 20 25 30

" Phe Lys Leu Ser Cys Met Pro Pro Asn Ser Thr Tyr Asp Tyr Phe Leu
" 35 40 45
"
" Leu Pro Ala Gly Leu Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr
" 50 55 60
"
" Glu Thr Ala Val Glu Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser
" 65 70 75 80
"
" Asn Leu Ser Lys Thr Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp
" 85 90 95
"
" Arg Asn Cys Ser Leu Cys Ala Asp Asn Ile Glu Gly Lys Thr Phe Val
" 100 105 110
"
" Ser Thr Val Asn Ser Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn
" 115 120 125
"
" Ile Gln Cys Trp Leu Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val
" 130 135 140
"
" Glu Ser Leu Phe Lys Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His
" 145 150 155 160
"
" Leu Leu Tyr Val Leu Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro
" 165 170 175
"
" Gln Lys Gly Ser Phe Gln Met Val His Cys Asn Cys Ser Val His Glu
" 180 185 190
"
" Cys Cys Glu Cys Leu Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr
" 195 200 205
"
" Leu Leu Met Cys Leu Lys Ile Thr Ser Gly Gly Val Ile Phe Gln Ser
" 210 215 220
"
" Pro Leu Met Ser Val Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro
" 225 230 235 240
"
" Leu Gly Leu His Met Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser
" 245 250 255
"
" Trp Ser Ser Pro Pro Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys
" 260 265 270
"
" Tyr Ser Glu Asn Ser Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val
" 275 280 285
"
" Ser Ala Thr Ser Leu Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr
" 290 295 300
"
" Glu Val Gln Val Arg Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser
" 305 310 315 320
"
" Asp Trp Ser Thr Pro Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe
" 325 330 335
"
" Pro Pro Lys Ile Leu Thr Ser Val Gly Ser Asn Val Ser Phe His Cys
" 340 345 350
"
" Ile Tyr Lys Lys Glu Asn Lys Ile Val Pro Ser Lys Glu Ile Val Trp
" 355 360 365
"
" Trp Met Asn Leu Ala Glu Lys Ile Pro Gln Ser Gln Tyr Asp Val Val

"" Gly Ala Ser Val Ala Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser
"" 725 730 735
"" Lys Val Asn Ile Val Gln Ser Leu Ser Ala Tyr Pro Leu Asn Ser Ser
"" 740 745 750
"" Cys Val Ile Val Ser Trp Ile Leu Ser Pro Ser Asp Tyr Lys Leu Met
"" 755 760 765
"" Tyr Phe Ile Ile Glu Trp Lys Asn Leu Asn Glu Asp Gly Glu Ile Lys
"" 770 775 780
"" Trp Leu Arg Ile Ser Ser Val Lys Lys Tyr Tyr Ile His Asp His
"" 785 790 795 800
"" Phe Ile Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Ile Phe Met
"" 805 810 815
"" Glu Gly Val Gly Lys Pro Lys Ile Ile Asn Ser Phe Thr Gln Asp Asp
"" 820 825 830
"" Ile Glu Lys His Gln Ser Asp Ala Gly Leu Tyr Val Ile Val Pro Val
"" 835 840 845
"" Ile Ile Ser Ser Ile Leu Leu Leu Gly Thr Leu Leu Ile Ser His
"" 850 855 860
"" Gln Arg Met Lys Lys Leu Phe Trp Glu Asp Val Pro Asn Pro Lys Asn
"" 865 870 875 880
"" Cys Ser Trp Ala Gln Gly Leu Asn Phe Gln Lys Pro Glu Thr Phe Glu
"" 885 890 895
"" His Leu Phe Ile Lys His Thr Ala Ser Val Thr Cys Gly Pro Leu Leu
"" 900 905 910
"" Leu Glu Pro Glu Thr Ile Ser Glu Asp Ile Ser Val Asp Thr Ser Trp
"" 915 920 925
"" Lys Asn Lys Asp Glu Met Met Pro Thr Thr Val Val Ser Leu Leu Ser
"" 930 935 940
"" Thr Thr Asp Leu Glu Lys Gly Ser Val Cys Ile Ser Asp Gln Phe Asn
"" 945 950 955 960
"" Ser Val Asn Phe Ser Glu Ala Glu Gly Thr Glu Val Thr Tyr Glu Ala
"" 965 970 975
"" Glu Ser Gln Arg Gln Pro Phe Val Lys Tyr Ala Thr Leu Ile Ser Asn
"" 980 985 990
"" Ser Lys Pro Ser Glu Thr Gly Glu Glu Gln Gly Leu Ile Asn Ser Ser
"" 995 1000 1005
"" Val Thr Lys Cys Phe Ser Ser Lys Asn Ser Pro Leu Lys Asp Ser Phe
"" 1010 1015 1020
"" Ser Asn Ser Ser Trp Glu Ile Glu Ala Gln Ala Phe Phe Ile Leu Ser
"" 1025 1030 1035 1040
"" Asp Gln His Pro Asn Ile Ile Ser Pro His Leu Thr Phe Ser Glu Gly
"" 1045 1050 1055

Leu Asp Glu Leu Leu Lys Leu Glu Gly Asn Phe Pro Glu Glu Asn Asn
1060 1065 1070

Asp Lys Lys Ser Ile Tyr Tyr Leu Gly Val Thr Ser Ile Lys Lys Arg
1075 1080 1085

Glu Ser Gly Val Leu Leu Thr Asp Lys Ser Arg Val Ser Cys Pro Phe
1090 1095 1100

Pro Ala Pro Cys Leu Phe Thr Asp Ile Arg Val Leu Gln Asp Ser Cys
1105 1110 1115 1120

Ser His Phe Val Glu Asn Asn Ile Asn Leu Gly Thr Ser Ser Lys Lys
1125 1130 1135

Thr Phe Ala Ser Tyr Met Pro Gln Phe Gln Thr Cys Ser Thr Gln Thr
1140 1145 1150

His Lys Ile Met Glu Asn Lys Met Cys Asp Leu Thr Val
1155 1160 1165

B
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